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AMENDMENTS TO THE CLAIMS:

Pursuant to 37 C.F.R. § 1.121, the following listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-87. (Canceled)

- 88. (Currently Amended) An interferon β polypeptide variant exhibiting interferon β activity, comprising a variant sequence which differs from the wild-type human interferon β sequence SEQ ID NO:2 in no more than 15 amino acid residues, the variant sequence comprising (a) at least one introduced N-glycosylation site comprising two amino acid substitutions relative to SEQ ID NO:2 selected from the group consisting of Q49N+Q51T/S and F111N+R113T/S, and (b) an amino acid substitution at position –1 relative to at least one of the introduced N-glycosylation site(s).
- 89. (Currently Amended) The variant according to claim 88, <u>further comprising</u>
 wherein at least one of the N-glycosylation site(s) is a naturally occurring N-glycosylation site.

90-91. (Canceled)

- 92. (Currently Amended) The variant according to claim <u>88</u> 90, wherein the variant comprises at least two introduced N-glycosylation sites.
 - 93. (Canceled)
- 94. (Previously Presented) The variant according to claim 88, further comprising at least one non-polypeptide moiety covalently attached to the variant.

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- 95. (Previously Presented) The variant according to claim 94, comprising at least one sugar moiety and at least one polymer molecule.
- 96. (Previously Presented) The variant according to claim 95, wherein at least one of the polymer molecule(s) is covalently attached to a lysine residue of the variant.
- 97. (Previously Presented) The variant according to claim 95, wherein at least one of the polymer molecule(s) is covalently attached to the N-terminus of the variant.
- 98. (Previously Presented) The variant according to claim 95, wherein the polymer molecule comprises a linear polyethylene glycol or a branched polyethylene glycol.
- 99. (Previously Presented) A composition comprising the variant of claim 88 or 94 and a pharmaceutically acceptable diluent, carrier, or excipient.

100-108. (Withdrawn)

- 109. (New) The variant according to claim 88, wherein the at least one introduced N-glycosylation site comprises substitutions Q49N+Q51T/S relative to SEQ ID NO:2.
- 110. (New) The variant according to claim 109, wherein the amino acid substitution at position -1 relative to the at least one introduced N-glycosylation site comprising substitutions Q49N+Q51T/S is selected from the group consisting of Q48F, Q48V, Q48W, and Q48Y.
- 111. (New) The variant according to claim 88, wherein the at least one introduced N-glycosylation site comprises substitutions F111N+R113T relative to SEQ ID NO:2.

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- 112. (New) The variant according to claim 111, wherein the amino acid substitution at position -1 relative to the at least one introduced N-glycosylation site comprising substitutions F111N+R113T/S is selected from the group consisting of D110F, D110V, D110W, and D110Y.
- 113. (New) The variant according to claim 112, wherein the amino acid substitution at position -1 relative to the at least one introduced N-glycosylation site comprising substitutions F111N+R113T/S is D110F.
- 114. (New) The variant according to claim 92, wherein the at least two introduced N-glycosylation sites comprise substitutions Q49N+Q51T and F111N+R113T.
- 115. (New) The variant according to claim 114, wherein the amino acid substitution at position -1 relative to the introduced N-glycosylation site comprising substitutions Q49N+Q51T is selected from the group consisting of Q48F, Q48V, Q48W, and Q48Y and the amino acid substitution at position -1 relative to the introduced N-glycosylation site comprising substitutions F111N+R113T is selected from the group consisting of D110F, D110V, D110W, and D110Y.
- 116. (New) The variant according to claim 88, further comprising the amino acid substitution C17S.
- 117. (New) The variant according to claim 115, further comprising the amino acid substitution C17S.